In [106]:

```python
# suppress display of warnings
import warnings
warnings.filterwarnings("ignore", category=DeprecationWarning)
warnings.filterwarnings("ignore", category=FutureWarning)

# 'Pandas' is used for data manipulation and analysis
import pandas as pd

# import subpackage of Matplotlib
import matplotlib.pyplot as plt

# import 'Seaborn'
import seaborn as sns

# 'Numpy' is used for mathematical operations on large, multi-dimensional arrays and matrices
import numpy as np

# 'Matplotlib' is a data visualization library for 2D and 3D plots, built on numpy
import matplotlib.pyplot as plt
import matplotlib.cm as cm
# train test split
from sklearn.model_selection import train_test_split

# 'StandardScalar' from sklearn.preprocessing library is used to scale the data
from sklearn.preprocessing import StandardScaler

# import various functions from sklearn
from sklearn.metrics import silhouette_score, silhouette_samples
from sklearn.cluster import KMeans

# 'eig' from numpy.linalg to calculate eigenvalues and eigenvectors
from numpy.linalg import eig

# 'PCA' function to perform principal component analysis using the sklearn library
from sklearn.decomposition import PCA

# 'LDA' function to perform linear discriminant analysis using the sklearn library
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA

# import decision tree classifier from sklearn
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, roc_auc_score

np.set_printoptions(suppress = True)

# import functions from sklearn to perform clustering
from sklearn.cluster import AgglomerativeClustering
from sklearn.metrics.pairwise import euclidean_distances
from sklearn.cluster import DBSCAN

# import functions from scipy to perform clustering
from scipy.cluster.hierarchy import linkage
from scipy.cluster.hierarchy import dendrogram
from scipy.cluster.hierarchy import cophenet
```

In [26]:

```python
df = pd.read_csv('dermatology.csv')
```

In [27]:

```python
df
```

Out[27]:

	erythema	Scaling	definite borders	itching	koebner phenomenon	polygonal papules	follicular papules	oral mucosal involvement	knee and elbow involvement	scalp involvement	...	disappearance of the granular layer	vacuolisat and dam of ba la
0	2	2	0	3	0	0	0	0	1	0	...	0	
1	3	3	3	2	1	0	0	0	1	1	...	0	
2	2	1	2	3	1	3	0	3	0	0	...	0	
3	2	2	2	0	0	0	0	0	3	2	...	3	
4	2	3	2	2	2	2	0	2	0	0	...	2	
...	...	...	...	...	...	...	...	...	...	...	...	...	
361	2	1	1	0	1	0	0	0	0	0	...	0	
362	3	2	1	0	1	0	0	0	0	0	...	1	
363	3	2	2	2	3	2	0	2	0	0	...	0	
364	2	1	3	1	2	3	0	2	0	0	...	0	
365	3	2	2	0	0	0	0	0	3	3	...	2	

366 rows × 35 columns

In [28]:
```
df.shape
```

Out[28]:
```
(366, 35)
```

In [29]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 366 entries, 0 to 365
Data columns (total 35 columns):
 #   Column                                    Non-Null Count  Dtype 
---  ------                                    --------------  ----- 
 0   erythema                                  366 non-null    int64 
 1   Scaling                                   366 non-null    int64 
 2   definite borders                          366 non-null    int64 
 3   itching                                   366 non-null    int64 
 4   koebner phenomenon                        366 non-null    int64 
 5   polygonal papules                         366 non-null    int64 
 6   follicular papules                        366 non-null    int64 
 7   oral mucosal involvement                  366 non-null    int64 
 8   knee and elbow involvement                366 non-null    int64 
 9   scalp involvement                         366 non-null    int64 
 10  family history                            366 non-null    int64 
 11  melanin incontinence                      366 non-null    int64 
 12  eosinophils in the infiltrate             366 non-null    int64 
 13  Unnamed: 13                               366 non-null    int64 
 14  PNL infiltrate                            366 non-null    int64 
 15  fibrosis of the papillary dermis          366 non-null    int64 
 16  exocytosis                                366 non-null    int64 
 17  acanthosis                                366 non-null    int64 
 18  hyperkeratosis                            366 non-null    int64 
 19  parakeratosis                             366 non-null    int64 
 20  clubbing of the rete ridges               366 non-null    int64 
 21  clubbing of the rete ridges.1             366 non-null    int64 
 22  thinning of the suprapapillary epidermis  366 non-null    int64 
 23  thinning of the suprapapillary epidermis.1 366 non-null    int64 
 24  focal hypergranulosis                     366 non-null    int64 
 25  disappearance of the granular layer       366 non-null    int64 
 26  vacuolisation and damage of basal layer   366 non-null    int64 
 27  spongiosis                                366 non-null    int64 
 28  saw-tooth appearance of retes             366 non-null    int64 
 29  follicular horn plug                      366 non-null    int64 
 30  perifollicular parakeratosis              366 non-null    int64 
 31  inflammatory monoluclear inflitrate       366 non-null    int64 
 32  band-like infiltrate                      366 non-null    int64 
 33  Age                                       366 non-null    object
 34  class label                               366 non-null    int64 
dtypes: int64(34), object(1)
memory usage: 100.2+ KB
```

In [30]:
```
df['Age'].isnull().sum()
```

Out[30]:
```
0
```

In [31]:
```
df = df[df['Age'] != '?']
```

In [32]:
```
df['Age'] = pd.to_numeric(df['Age'], errors='coerce')
```

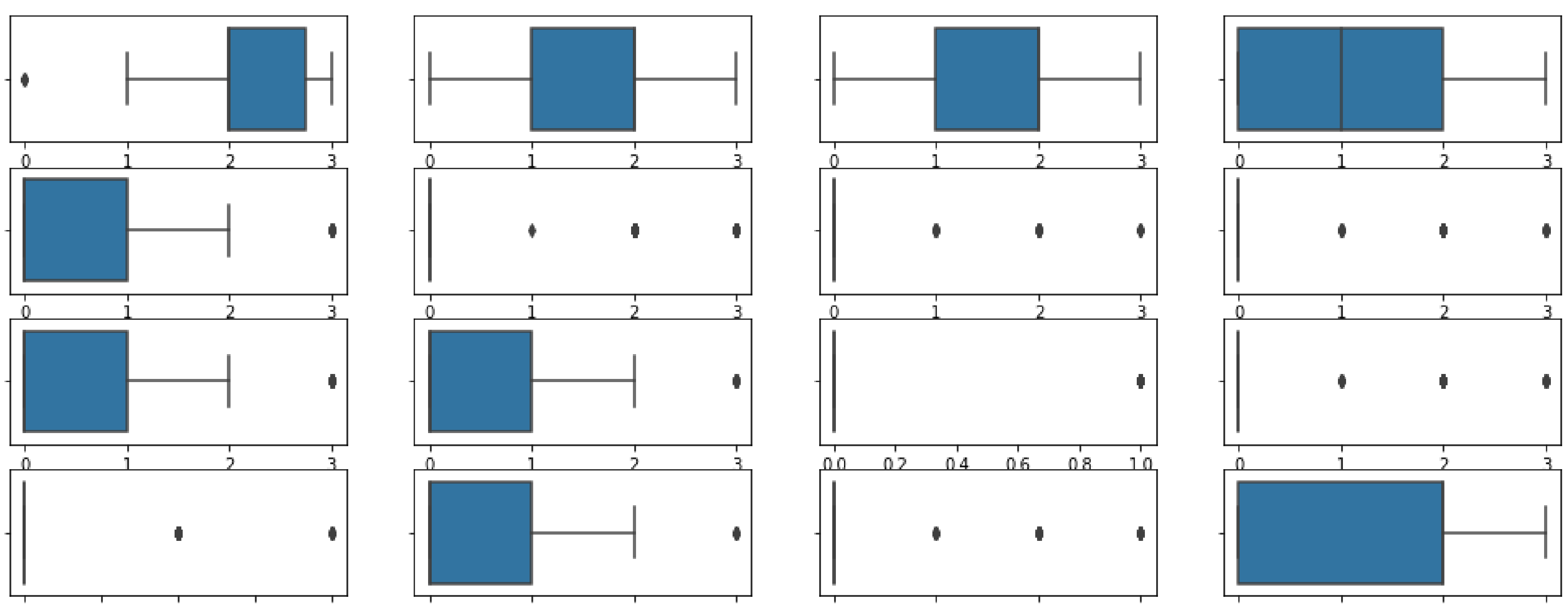
```
C:\Users\naras\AppData\Local\Temp\ipykernel_1788\1391001171.py:1: SettingWithCopyWarning: 
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)
  df['Age'] = pd.to_numeric(df['Age'], errors='coerce')
```

In [33]:
```python
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 358 entries, 0 to 365
Data columns (total 35 columns):
 #   Column                                   Non-Null Count  Dtype
---  ------                                   --------------  -----
 0   erythema                                 358 non-null    int64
 1   Scaling                                  358 non-null    int64
 2   definite borders                         358 non-null    int64
 3   itching                                  358 non-null    int64
 4   koebner phenomenon                       358 non-null    int64
 5   polygonal papules                        358 non-null    int64
 6   follicular papules                       358 non-null    int64
 7   oral mucosal involvement                 358 non-null    int64
 8   knee and elbow involvement               358 non-null    int64
 9   scalp involvement                        358 non-null    int64
 10  family history                           358 non-null    int64
 11  melanin incontinence                     358 non-null    int64
 12  eosinophils in the infiltrate            358 non-null    int64
 13  Unnamed: 13                              358 non-null    int64
 14  PNL infiltrate                           358 non-null    int64
 15  fibrosis of the papillary dermis         358 non-null    int64
 16  exocytosis                               358 non-null    int64
 17  acanthosis                               358 non-null    int64
 18  hyperkeratosis                           358 non-null    int64
 19  parakeratosis                            358 non-null    int64
 20  clubbing of the rete ridges              358 non-null    int64
 21  clubbing of the rete ridges.1            358 non-null    int64
 22  thinning of the suprapapillary epidermis 358 non-null    int64
 23  thinning of the suprapapillary epidermis.1 358 non-null  int64
 24  focal hypergranulosis                    358 non-null    int64
 25  disappearance of the granular layer      358 non-null    int64
 26  vacuolisation and damage of basal layer  358 non-null    int64
 27  spongiosis                               358 non-null    int64
 28  saw-tooth appearance of retes            358 non-null    int64
 29  follicular horn plug                     358 non-null    int64
 30  perifollicular parakeratosis             358 non-null    int64
 31  inflammatory monoluclear inflitrate      358 non-null    int64
 32  band-like infiltrate                     358 non-null    int64
 33  Age                                      358 non-null    int64
 34  class label                              358 non-null    int64
dtypes: int64(35)
memory usage: 100.7 KB
```

In [34]:
```python
df_clm = df.columns
```

In [35]:
```python
t=1
plt.figure(figsize = (17,15))
for i in df_clm:
    plt.subplot(9,4,t)
    sns.boxplot(df[i])
    t+=1
plt.show()
```



In [36]:
```python
# for i in df_clm:
#     q1,q3 = np.quantile(df[i],[0.25,0.75])
#     iqr = q3 - q1
#     ub = q3 + (1.5 * iqr)
#     lb = q1 - (1.5 * iqr)
#     df[i] = np.where(df[i] > ub, ub, df[i])
#     df[i] = np.where(df[i] < lb, lb, df[i])
```

In [37]:
```python
# t=1
# plt.figure(figsize = (17,15))
# for i in df_clm:
#     plt.subplot(9,4,t)
#     sns.boxplot(df[i])
#     t+=1
# plt.show()
```

In [38]:
```python
df.corr()
```

Out[38]:

	erythema	Scaling	definite borders	itching	koebner phenomenon	polygonal papules	follicular papules	oral mucosal involvement	knee and elbow involvement	scalp involvement	...	dis of t
erythema	1.000000	0.428769	0.248062	-0.033157	-0.008496	0.028225	-0.115275	-0.033391	0.138519	0.180740	...	
Scaling	0.428769	1.000000	0.347106	-0.072191	-0.009033	-0.075013	-0.098665	-0.084815	0.294258	0.295932	...	
definite borders	0.248062	0.347106	1.000000	-0.058534	0.239778	0.322657	-0.176715	0.280341	0.301187	0.261495	...	
itching	-0.033157	-0.072191	-0.058534	1.000000	0.280039	0.412525	-0.144027	0.361761	-0.296824	-0.152562	...	
koebner phenomenon	-0.008496	-0.009033	0.239778	0.280039	1.000000	0.388233	-0.175676	0.387937	-0.065438	0.013496	...	
polygonal papules	0.028225	-0.075013	0.322657	0.412525	0.388233	1.000000	-0.139384	0.863269	-0.278843	-0.258231	...	
follicular papules	-0.115275	-0.098665	-0.176715	-0.144027	-0.175676	-0.139384	1.000000	-0.134484	0.220849	-0.007320	...	
oral mucosal	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]		

In [41]:
```python
plt.figure(figsize=(20, 20))
sns.heatmap(df.corr(),annot = True)
```

Out[41]: <AxesSubplot:>

In [49]:
```python
# sns.pairplot(df)
```

In [43]:
```python
cov_mat = np.cov(df.T)
print(cov_mat[0:5])
```

```
[[ 0.44204497  0.19999061  0.14858457 -0.0250223  -0.00513278  0.01794908
  -0.04417633 -0.01859068  0.09120073  0.10963492  0.03797944  0.02101623
   0.01963914  0.1195249  -0.18442014  0.01870022  0.03991988 -0.02048417
   0.13149617  0.11614478  0.01812121  0.11207612  0.07739856  0.05511478
  -0.01172089  0.08880647 -0.00253509  0.02915356 -0.00791825 -0.00272288
   0.00200304  0.04325306 -0.01020296 -0.0512339  -0.34425614]
 [ 0.19999061  0.49215999  0.21937937 -0.05748556 -0.00575873 -0.0503341
  -0.03989641 -0.04982552  0.20442702  0.18941208  0.0433626  -0.04948907
   0.0107272   0.1562368  -0.2163044  -0.08279736  0.06138992  0.01756569
   0.19846486  0.24279768  0.12561226  0.23621739  0.14180085  0.09647434
  -0.05444971  0.12539317 -0.07618578  0.01829335 -0.07952678 -0.00469462
  -0.00533621 -0.00414691 -0.104909    0.1720733  -0.51269893]
 [ 0.14858457  0.21937937  0.81163639 -0.05985634  0.19629751  0.27803077
  -0.09176408  0.21149242  0.26870413  0.21493514  0.03341001  0.2415536
  -0.05339342  0.02608641 -0.18877048 -0.21069433  0.1347824   0.04963773
   0.30618281  0.38081154  0.23646777  0.34436568  0.15133875  0.16465581
   0.21992708  0.27486972  0.25203825 -0.25698324  0.23122545 -0.03824547
  -0.05863574  0.07863481  0.2746037   1.91203856 -0.54776771]
 [-0.0250223  -0.05748556 -0.05985634  1.28836674  0.28884403  0.44785847
```

In [44]:
```python
# use 'eig' function to compute eigenvalues and eigenvectors of the covariance matrix
eig_val, eig_vec = np.linalg.eig(cov_mat)

print('Eigenvalues:','\n','\n', eig_val,"\n")

print('Eigenvectors:','\n','\n',eig_vec,'\n')
```

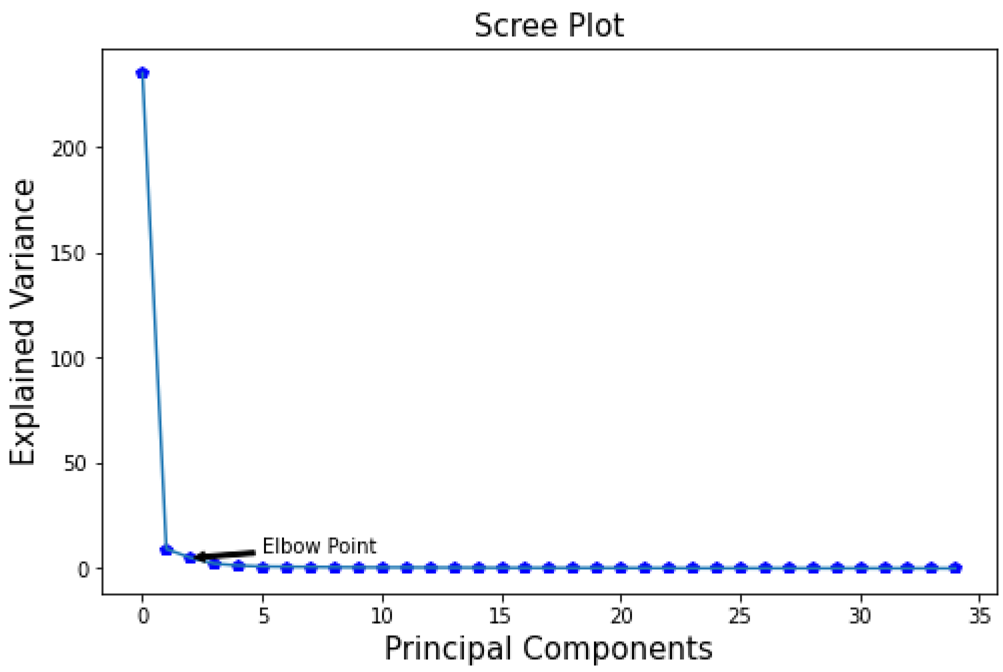
```
Eigenvalues:

 [235.3300678    9.24592823   5.12808939   2.3148928    1.4024016
   0.91337358   0.81042609   0.71593857   0.60095368   0.55235077
   0.50813846   0.49553053   0.44101188   0.38419379   0.35734125
   0.30619828   0.26523004   0.25767359   0.23909006   0.22446452
   0.20956021   0.01308496   0.17067294   0.15233829   0.03857301
   0.05231658   0.06523876   0.06854187   0.07311938   0.08012027
   0.1130052    0.10812021   0.09245087   0.09900721   0.09605179]

Eigenvectors:

 [[-0.0001554   0.03505206  0.07095608 ... -0.02619762  0.01355569
   0.01395414]
 [ 0.00081883  0.07663563  0.08343331 ... -0.00267301 -0.05716716
   0.05304328]
 [ 0.00833426  0.05138318  0.24954831 ... -0.03640348  0.05732959
   0.07456333]
 ...
```

In [45]:
```python
# create a list of eigenvalues
eig_val = list(eig_val)

# 'sort(reverse = True)' will sort the eigenvalues in the descending order
eig_val.sort(reverse = True)

# print the sorted list
print(eig_val)
```

```
[235.33006779519386, 9.245928230012801, 5.128089388280847, 2.314892796543686, 1.4024016009885227, 0.913373576594056
4, 0.8104260859712394, 0.7159385715037455, 0.6009536828739348, 0.5523507728773607, 0.5081384552739516, 0.49553052934
30893, 0.4410118768284154, 0.38419378898035994, 0.35734125135657596, 0.3061982839045628, 0.26523004146976875, 0.2576
735921871564, 0.2390900601961843, 0.22446452153922375, 0.20956021365882846, 0.17067294323373322, 0.1523382889439162
4, 0.11300519637264449, 0.10812020517926119, 0.0990072072390541, 0.09605179370302686, 0.092450871804987, 0.080120268
62579272, 0.07311938359999973, 0.06854187117742573, 0.06523875545825317, 0.052316579256128856, 0.03857301361992849,
0.01308496177317094]
```

a) **Kaiser criterion** : This criterion considers the number of pricipal components for which the eigenvalue is greater than 1. This criterion suffers a drawback of selecting more number of components as the eigenvalues very close to 1 may not contribute significantly in explaining the variation in the data. Here the first five eigenvalues are greater than 1. Thus we can consider 5 principal components using kaiser criterion.

In [65]:
```python
plt.figure(figsize=(8, 5))
plt.plot(eig_val,'bp')
plt.plot(eig_val)
plt.title('Scree Plot', fontsize = 15)
plt.xlabel('Principal Components', fontsize = 15)
plt.ylabel('Explained Variance', fontsize = 15)
plt.annotate(text='Elbow Point', xy=(2,5), xytext=(5,7), arrowprops=dict(facecolor='black', arrowstyle = 'simple'))
plt.show()
```



Interpretation: It can be observed that, after the elbow point, the principal components do not contribute much to the variance in the data. The Kaiser criterion considers the number of principal components as 5, but the scree plot shows that only first three components explains most of the variation.

In [97]:
```
#c Percentage of Explained Variation
percent_var = []
for i in eig_val:
    variation = (i/sum(eig_val))*100
    percent_var.append(variation)

print(percent_var)
```

```
 0.18918758809230837,
 0.16837302316738414,
 0.146680561525837,
 0.13642858606443348,
 0.11690281704076404,
 0.10126163548754169,
 0.09837667415889369,
 0.09128170545884401,
 0.08569785094491672,
 0.08000756569888924,
 0.06516087419640991,
 0.05816092400525799,
 0.043144022976707525,
 0.04127899217234213,
 0.03779975931279763,
 0.03667141801879588,
 0.035296629406473545,
 0.03058895361849003,
 0.027916100032057807,
 0.026168460919211628,
```

Interpretation: It can be seen that the first principal component explains 89.84% variation in the data.

In [67]:
```
np.cumsum(percent_var)
```

Out[67]:
```
array([ 89.84618564,  93.37616969,  95.33401245,  96.21781064,
        96.75323069,  97.10194572,  97.41135664,  97.68469336,
        97.91413024,  98.12501111,  98.31901225,  98.50819984,
        98.67657287,  98.82325343,  98.95968201,  99.07658483,
        99.17784647,  99.27622314,  99.36750484,  99.4532027 ,
        99.53321026,  99.59837114,  99.65653206,  99.69967608,
        99.74095507,  99.77875483,  99.81542625,  99.85072288,
        99.88131184,  99.90922794,  99.9353964 ,  99.96030377,
        99.98027761,  99.99500432, 100.        ])
```

In [98]:
```
pca = PCA(n_components = 5, random_state = 10)
components = pca.fit_transform(df)
```

In [99]:
```
df_pca = pd.DataFrame(data = components, columns = ['PC1', 'PC2', 'PC3', 'PC4', 'PC5'])
df_pca.head()
```

Out[99]:

	PC1	PC2	PC3	PC4	PC5
0	18.621655	-1.460772	-2.478290	-2.322577	-1.266360
1	-28.174714	3.529331	2.591427	-0.663806	-1.391516
2	-10.225587	-4.342322	3.415217	-0.007982	-0.429869
3	3.803523	4.939282	1.644943	-0.470654	1.374029
4	8.778375	-4.154797	3.028559	0.089421	0.573878

In [100]:
```
df_pca.shape
```

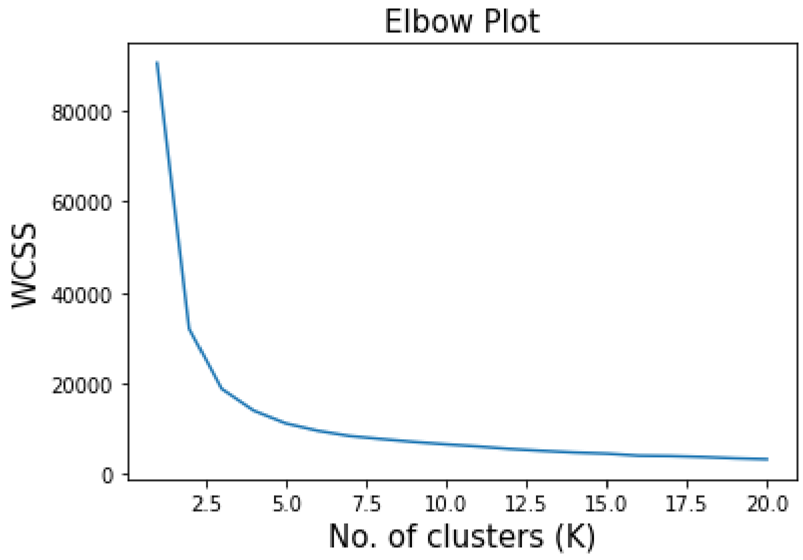
Out[100]:
```
(358, 5)
```

*Interpretation**: In the above step, we obtained the data with reduced dimensions. The new dataset has 358 observations and 5 columns, i.e. we have decreased the number of features from 33 to 5.

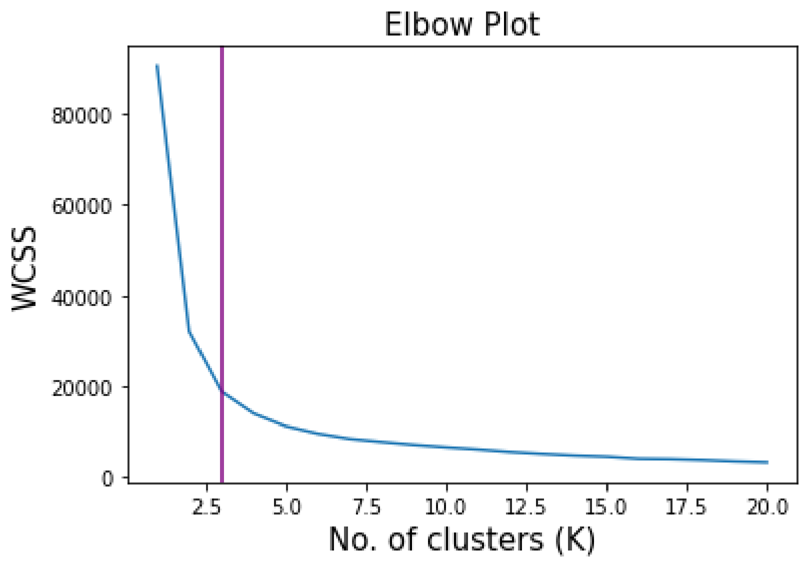
K Mean clustering

In [101]:
```
wcss  = []

for i in range(1,21):
    kmeans = KMeans(n_clusters = i, random_state = 10)
    kmeans.fit(df_pca)
    wcss.append(kmeans.inertia_)
```

In [102]:
```
plt.plot(range(1,21), wcss)

plt.title('Elbow Plot', fontsize = 15)
plt.xlabel('No. of clusters (K)', fontsize = 15)
plt.ylabel('WCSS', fontsize = 15)

plt.show()
```



In [103]:
```
plt.plot(range(1,21), wcss)

# set the axes and plot labels
# set the font size using 'fontsize'
plt.title('Elbow Plot', fontsize = 15)
plt.xlabel('No. of clusters (K)', fontsize = 15)
plt.ylabel('WCSS', fontsize = 15)

# plot a vertical line at the elbow
plt.axvline(x = 3, color = 'purple')

# display the plot
plt.show()
```



Interpretation: We can see that the for K = 3, there is an elbow in the plot. Before this elbow point, the WCSS is decreasing rapidly and after K = 3, the WCSS is decreasing slowly.

Now, let us use the silhouette score method to identify the optimal value of K.

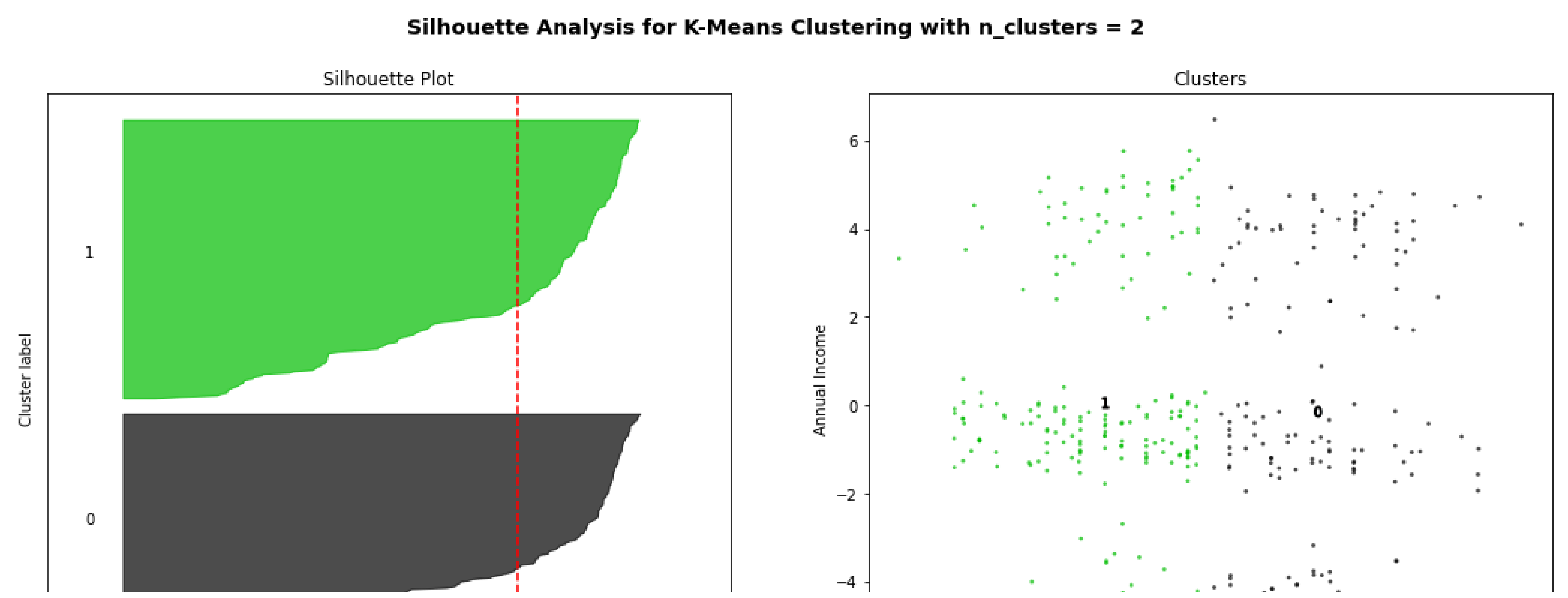
Optimal Value of K Using Silhouette Score

In [104]:
```
n_clusters = [2, 3, 4]

for K in n_clusters:
    cluster = KMeans (n_clusters= K, random_state= 10)
    predict = cluster.fit_predict(df_pca)
    score = silhouette_score(df_pca, predict, random_state= 10)
    print ("For {} clusters the silhouette score is {})".format(K, score))
```

```
For 2 clusters the silhouette score is 0.5191697623265723)
For 3 clusters the silhouette score is 0.43779531499250857)
For 4 clusters the silhouette score is 0.38576744970658744)
```

In [107]:

```
n_clusters = [2,3,4]
X = np.array(df_pca)

for K in n_clusters:
    fig, (ax1, ax2) = plt.subplots(1, 2)
    fig.set_size_inches(18, 7)
    model = KMeans(n_clusters = K, random_state = 10)
    cluster_labels = model.fit_predict(X)
    silhouette_avg = silhouette_score(X, cluster_labels)
    sample_silhouette_values = silhouette_samples(X, cluster_labels)
    y_lower = 10
    for i in range(K):
        ith_cluster_silhouette_values = sample_silhouette_values[cluster_labels == i]
        ith_cluster_silhouette_values.sort()
        size_cluster_i = ith_cluster_silhouette_values.shape[0]
        y_upper = y_lower + size_cluster_i
        color = cm.nipy_spectral(float(i) / K)
        ax1.fill_betweenx(np.arange(y_lower, y_upper),
                          0, ith_cluster_silhouette_values,
                          facecolor=color, edgecolor=color, alpha=0.7)
        ax1.text(-0.05, y_lower + 0.5 * size_cluster_i, str(i))
        y_lower = y_upper + 10

    ax1.set_title("Silhouette Plot")
    ax1.set_xlabel("Silhouette coefficient")
    ax1.set_ylabel("Cluster label")
    ax1.axvline(x=silhouette_avg, color="red", linestyle="--")
    ax1.set_yticks([])
    ax1.set_xticks([-0.1, 0, 0.2, 0.4, 0.6, 0.8])
    colors = cm.nipy_spectral(cluster_labels.astype(float) / K)
    ax2.scatter(X[:, 0], X[:, 1], marker='.', s=30, lw=0, alpha=0.7, c=colors, edgecolor='k')
    centers = model.cluster_centers_

    for i, c in enumerate(centers):
        ax2.scatter(c[0], c[1], marker='$%d$' % i, alpha=1, s=50, edgecolor='k')

    ax2.set_title("Clusters")
    ax2.set_xlabel("Spending Score")
    ax2.set_ylabel("Annual Income")
    plt.suptitle(("Silhouette Analysis for K-Means Clustering with n_clusters = %d" % K), fontsize=14,fontweight='bold

plt.show()
```



In [108]:

```
# build a K-Means model with 5 clusters
new_clust = KMeans(n_clusters = 3, random_state = 10)
new_clust.fit(df_pca)
df_pca['Cluster'] = new_clust.labels_
```

In [109]:

```
df_pca.head()
```

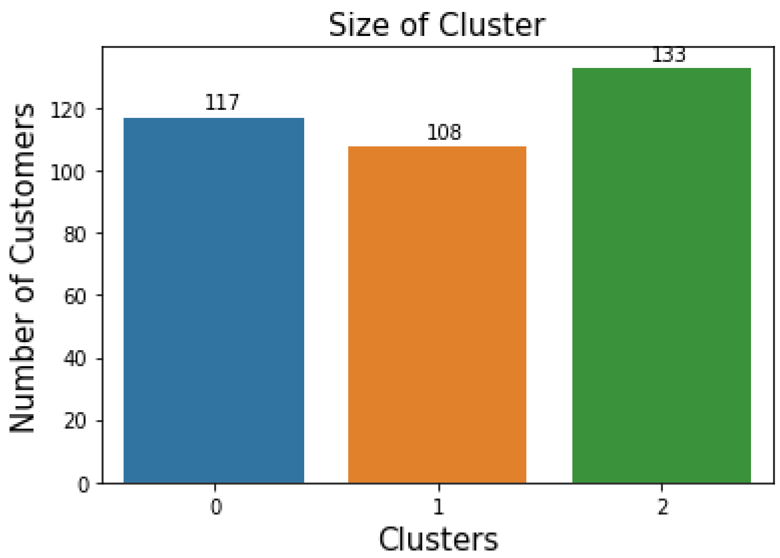
Out[109]:

	PC1	PC2	PC3	PC4	PC5	Cluster
0	18.621655	-1.460772	-2.478290	-2.322577	-1.266360	1
1	-28.174714	3.529331	2.591427	-0.663806	-1.391516	0
2	-10.225587	-4.342322	3.415217	-0.007982	-0.429869	0
3	3.803523	4.939282	1.644943	-0.470654	1.374029	2
4	8.778375	-4.154797	3.028559	0.089421	0.573878	2

In [110]:
```
df_pca.Cluster.value_counts()
```

Out[110]:
```
2    133
0    117
1    108
Name: Cluster, dtype: int64
```

In [113]:
```
sns.countplot(data= df_pca, x = 'Cluster')

plt.title('Size of Cluster', fontsize = 15)
plt.xlabel('Clusters', fontsize = 15)
plt.ylabel('Number of Customers', fontsize = 15)

plt.text(x = -0.05, y =120, s = np.unique(new_clust.labels_, return_counts=True)[1][0])
plt.text(x = 0.95, y =110, s = np.unique(new_clust.labels_, return_counts=True)[1][1])
plt.text(x = 1.95, y =135, s = np.unique(new_clust.labels_, return_counts=True)[1][2])

plt.show()
```



Cluster 2

In [114]:
```
len(df_pca[df_pca['Cluster'] == 0])
```

Out[114]: 117

In [115]:
```
df_pca[df_pca.Cluster==0].describe()
```

Out[115]:

	PC1	PC2	PC3	PC4	PC5	Cluster
count	117.000000	117.000000	117.000000	117.000000	117.000000	117.0
mean	-17.214156	0.147050	-0.101684	0.030931	-0.014660	0.0
std	6.484203	2.643979	2.169630	1.583982	1.530397	0.0
min	-36.185988	-5.216786	-2.916642	-3.009619	-2.436768	0.0
25%	-20.371583	-1.055989	-1.975199	-0.984834	-1.106908	0.0
50%	-16.203222	-0.402629	-0.942475	-0.062758	-0.204593	0.0
75%	-11.370593	2.411305	2.052546	0.850162	0.749274	0.0
max	-9.145142	5.763745	4.841648	3.521551	4.158952	0.0

Cluster 3

In [116]:
```
len(df_pca[df_pca['Cluster'] == 1])
```

Out[116]: 108

In [117]:
```
df_pca[df_pca.Cluster==1].describe()
```

Out[117]:

	PC1	PC2	PC3	PC4	PC5	Cluster
count	108.000000	108.000000	108.000000	108.000000	108.000000	108.0
mean	18.497437	0.048628	-0.206381	0.134282	0.159249	1.0
std	6.449455	3.285000	2.237127	1.503778	0.939867	0.0
min	9.595671	-5.255957	-4.359619	-2.833962	-1.849703	1.0
25%	13.766860	-1.774869	-2.488028	-0.760424	-0.614765	1.0
50%	16.771569	-0.764789	0.428883	0.121590	0.263227	1.0
75%	23.721249	3.587507	1.379537	0.845071	0.942149	1.0
max	38.774204	4.830898	3.761979	3.626998	1.800975	1.0

Cluster 4

In [118]:
```
len(df_pca[df_pca['Cluster'] == 2])
```

Out[118]:
```
133
```

In [119]:
```
df_pca[df_pca.Cluster==2].describe()
```

Out[119]:

	PC1	PC2	PC3	PC4	PC5	Cluster
count	133.000000	133.000000	133.000000	133.000000	133.000000	133.0
mean	0.122805	-0.168847	0.257039	-0.136251	-0.116418	2.0
std	4.814646	3.172617	2.359022	1.479353	0.991963	0.0
min	-8.368177	-5.267542	-3.531863	-3.175788	-2.609816	2.0
25%	-3.325839	-1.418854	-1.973046	-1.004968	-0.871150	2.0
50%	-0.374583	-0.677704	0.337039	-0.141694	0.066852	2.0
75%	3.774034	2.831841	2.238309	0.556180	0.589770	2.0
max	8.809992	6.480041	4.306348	3.710399	1.543585	2.0

In [ ]:
```

```